

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: August 23, 2003, 18:23:39 ; Search time 67 Seconds
(without alignments)
2305.733 Million cell updates/sec

Title: US-09-745-506-37
Perfect score: 1799
Sequence: 1 MDKALLSLINDFASLSFAE.....LENNKINILSETDRPLQVY 350

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human4.0.cdl
-LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-NO_MAP -LARGEQUERY -NBG_SCORES=0 -WAIT -DSBPLCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FPAEXT=7 -FGAPOP=10 -YGAEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA.*

- 1: /cgcn2.6/ptodata/2/ina/5a.COMB.seq.*
- 2: /cgcn2.6/ptodata/2/ina/5b.COMB.seq.*
- 3: /cgcn2.6/ptodata/2/ina/5a.COMB.seq.*
- 4: /cgcn2.6/ptodata/2/ina/5b.COMB.seq.*
- 5: /cgcn2.6/ptodata/2/ina/PTDS.COMB.seq.*
- 6: /cgcn2.6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	320.5	17.8	1137	4	US-09-107-532A-1088
2	305	17.0	1104	4	US-09-134-001C-841
3	253	14.1	5463	4	US-09-221-017B-610
4	216.5	12.0	4411529	3	US-09-103-840A-1
5	203.5	11.3	13206	4	US-08-961-527-33
6	191	10.6	1664976	4	US-08-916-421B-1
7	171.5	9.5	4403765	3	US-09-103-840A-2
8	106	5.9	771	4	US-09-252-991A-8080
9	106	5.9	888	4	US-09-252-991A-8235
10	104	5.8	789	4	US-09-328-352-356
11	101	5.6	3428	4	US-09-146-053-1
12	101	5.6	3428	4	US-10-002-593-9

13	100	5.6	1767	4	US-09-328-352-3868	Sequence 3868, App
14	97.5	5.4	969	4	US-09-252-991A-12362	Sequence 12362, A
15	97.5	5.4	1530	4	US-09-252-991A-12109	Sequence 12109, A
16	97.5	5.4	2091	4	US-09-252-991A-12312	Sequence 12312, A
17	94.5	5.3	1230025	4	US-09-198-452A-1	Sequence 1, Appl1
18	94	5.2	4215	4	US-09-620-312D-295	Sequence 295, App
19	92.5	5.1	8411	4	US-08-961-527-16	Sequence 16, Appl
20	92	5.1	2415	4	US-09-134-001C-2381	Sequence 2381, App
21	91.5	5.1	678	4	US-09-252-991A-12248	Sequence 12248, A
22	91.5	5.1	1219	4	US-08-936-165A-52	Sequence 52, Appl1
23	91.5	5.1	1664976	4	US-08-916-421B-1	Sequence 1, Appl1
24	91	5.1	2208	4	US-09-134-001C-603	Sequence 603, App
25	91	5.1	1830121	4	US-09-557-884-1	Sequence 1, Appl1
26	91	5.1	1830121	4	US-09-557-884-1	Sequence 1, Appl1
27	91	5.1	1830121	4	US-09-643-990A-1	Sequence 1, Appl1
28	91	5.1	1830121	4	US-09-643-990A-1	Sequence 1, Appl1
29	90	5.0	1788	4	US-09-328-352-306	Sequence 306, App
30	90	5.0	3177	4	US-09-328-352-150	Sequence 150, App
31	89.5	5.0	2310	4	US-09-854-856-43	Sequence 43, Appl
32	89.5	5.0	2490	4	US-09-854-856-11	Sequence 11, Appl
33	89.5	5.0	2769	4	US-09-854-856-37	Sequence 37, Appl
34	89.5	5.0	2949	4	US-09-854-856-3	Sequence 5, Appl1
35	89.5	5.0	5820	4	US-09-854-856-47	Sequence 4, Appl
36	89.5	5.0	6000	4	US-09-854-856-15	Sequence 15, Appl
37	89.5	5.0	6099	4	US-09-854-856-41	Sequence 41, Appl
38	89.5	5.0	6231	4	US-09-854-856-45	Sequence 45, Appl
39	89.5	5.0	6279	4	US-09-854-856-9	Sequence 9, Appl1
40	89.5	5.0	6411	4	US-09-854-856-13	Sequence 13, Appl
41	89.5	5.0	6510	4	US-09-854-856-39	Sequence 39, Appl
42	89.5	5.0	6558	4	US-09-854-856-35	Sequence 35, Appl
43	89.5	5.0	6690	4	US-09-854-856-7	Sequence 7, Appl1
44	89.5	5.0	6738	4	US-09-854-856-3	Sequence 3, Appl1
45	89.5	5.0	6969	4	US-09-854-856-33	Sequence 33, Appl1

ALIGNMENTS

RESULT 1
US-09-107-532A-1088
; Sequence 1088, Application US/09107532A
; Patent No. 6583275
GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham,
; STATE: Massachusetts
; COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCI
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
; NAME: Arinello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277

```

? INFORMATION FOR SEQ ID NO: 1088:
?   SEQUENCE CHARACTERISTICS:
?       LENGTH: 1137 base pairs
?       TYPE: nucleic acid
?       STRANDEDNESS: double
?       TOPOLOGY: circular
?       MOLECULE TYPE: DNA (genomic)
?       HYPOTHETICAL: NO
?       ANTI-SENSE: NO
?       ORIGINAL SOURCE:
?           ORGANISM: Enterococcus faecium
?
? FEATURE:
?     NAME/KEY: misc_feature
?     LOCATION: (B) LOCATION 1...1137
?     SEQUENCE DESCRIPTION: SEQ ID NO: 1088:
US-09-107-532A-1088

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Alignment Scores:
Pred. No.:      8,86e-30          Length:      1137
Score:          320.50            Matches:     100
Percent Similarity: 45.36%        Conservative: 81
Best Local Similarity: 25.06%     Mismatches:  131
Query Match:    17.82%            Indels:      87
Db:             4                 Gaps:         16

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US-09-745-506-37 (1-350) x US-09-107-532A-1088 (1-1137)
Oy      4 LysAlaLeuSerSeTyrLeuAsnAspPheAlaSerLeuSerPheAlaGluSerTrpasp 23
      ::      ::      ::      ::      ::      ::      |||||
Db      31 CGCAGCTTCATCCAAAGTTTAAAGCTATTGTCCCACTGGCTAGCTGACAGAAGAC 90
      .      .      .      .      .      .      .
Oy      24 AsnValGlyLeu-----LeuValGluProSerProProHisThrValAsnThr 39
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
      91 CCAGCGGAGCTGCATATCGGAACAATTGGATTAGCCA-----ATCCAACGA 135
      .
Oy      40 LeuPheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGlnIleuSylsala 59
      ::      ::      ::      ::      ::      ::      |||||::|||::|||::|||::|||::|||::|||
Db      136 GTAATGATGACACTTGACCTTCGTCACAGAAGTGTCTGGAAAGACATCAAGAAAAATC 195
      .
Oy      60 AspLeuIleLeuSerTyrHisProProIlePheArgPrometLysArgIleThrTrpasn 79
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      196 GATTTGCGATGCTCAAAACATCTCCAACTTTCGCTCGTAATAAACGGCTGGTTACTGAT 255
      .
Oy      80 ThrTrpLysGluArgLeuValIleArgAlaLeuGluAsnArgValGlyIleTyrSerpro 99
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      256 CAGCCACAGAAAATGATGATGACAGATTGTGTAACAAGATATGCCGCTATGACGA 315
      .
Oy      100 HisThrAlaTyrAspAlaAlaLeuProGlnGlyValAsnAsnTrpLeuAlaLysGlyLeuGly 119
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      316 CACACGAAACATGATATTATTGTGGATGACAGCAATGACGTGGTTGTGAACCTTCGGT 375
      .
Oy      120 -----AlaCysThrSerArgProIleHisProSerLysAlaLaproasn 133
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      376 ATTAGAGTGGAGAGATTATTACTTAAGACTCATGATGACATCATTAATAAAAAACGGCCGT 435
      .
Oy      134 TyrProThrGluGlyAsnHisArgValGluPheAsnValAsnTyrrhgInaspleuasp 153
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      436 TAT-----GTAACCtGTGATCATGCACGAAAAATGCC 168
      .
Oy      154 LysValMetSerAlaValLysGly-----IleaspGlyValSerValThr 168
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      469 GAAGATATTAGTCGACGCTGCTGTCACACAAGGTATATACCGGTACAAATTATAC 528
      .
Oy      169 SerPheSer-----AlaargThr 174
      |||||
Db      539 TCAGATTGGACACGCTCGATTACTCCGGAAGCTGTGCACAAACCACGCGATTGGGAAAGTA 588
      .
Oy      175 GlYasnGluGluGlnThrArgIleAsnLeuAsnCysThrGlnLysAlaLeuMetGlnVal 194
      |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      589 GGGAAGACAGACAAA-----GTTCAAAGAGCAAAGTAAGTTGAGGTT 627
      .
Oy      195 ValAspPheLeuSerArgAsnLysGlnLeuTyrGlnLysThr----- 208
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

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Db      628  ATTTCGGCGAAACATACGAAAAAACAAGTGTCTCAACGCCATGCGGTACGCTCATCCTTAT 687
Qy      209  -----GullileuSerLeuGluIysProleuLeuHisThiGlyMet 223
Db      688  GAGGAACCTCGCTTATGATCTTTTCGTATKATATACACAGCAAGAAAGTTT--GGGTTA 744
Qy      224  G1yArGLeuCyStrhIleAspGluSerValSerIleuAlaThrMetIleAspArgIleLys 243
Db      745  GGACGAGTAGTGAATTTGCCGCAAGAAATTTTATAGAGCGCATTTGTAAACAAGTAAAA 804
Qy      244  ArgHisIysLeuSerHisIleArgLeuAlaLeuGlyAlaGlyThrLeuGluSer 263
Db      805  GAACGCTTCCACATGATGACATGAGATATGTC-----CAGCCAAAAAATGCAAAATCC 858
Qy      264  GlnAllyValValAlaLeuCyAlaGlySerGly-----SerSerVal 278
Db      859  TCTGTGAAGCCCATTCGCGATTCGCGTGGAGGCGGTGAAAAATTTTATCCGCAAGCATC 918
Qy      279  LeuGlnGlyValGluAlaAspLeuTyrLeuThrGlyGlnMetSerHisAspThrLeu 298
Db      919  GCCCAA-----AGACGATGATCTATATACCGGAGATATCTATATCATACGCGTCAT 972
Qy      299  AspAlaAlaSerGlnGlyIleAsnValIle-----LeuCys 310
Db      973  GATATGCCAAACGCTGGGTGATTCATCATATGATCCGCTCATATATTTGAATCGTATAGC 1032
Qy      311  GlnHisSerAsnThrGluArgGlyPheLeuSerAspLeuArgAspMetLeuAspSerHis 330
Db      1093  AAGCAAGCATTTATCGAGAAA--TTTGAATCTTGGAACAAAGAAA----- 1074
Qy      331  LeuGlnAsn--LysIleAsnIleIleLeuSerGluThrAspArgAspProLeuGln 348
Db      1075  --GAAAAATTGGATATTAACTTTGCTTGTGAACAATAACAAACCACTTTGCA 1128

RESULT 2
US-09-134-001C-841
; Sequence 841, Application us/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 841
; LENGTH: 1104
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-841

Alignment Scores:
Pred. No.: 7,06e-28 Length: 1104
Score: 305.00 Matches: 96
Percent Similarity: 43.54% Conservative: 76
Best local Similarity: 24.30% Mismatch: 145
Query Match: 16.95% Indels: 78
DB: 4 Gaps: 13

US-09-745-506-37 (1-350) x US-09-134-001C-841 (1-1104)
Qy      1  MetaspLeuLysAlaLeuLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGlu 20
Db      4  ATGAAATTAAGTGAACATGATGAGAGTTTAAATATATACAGTTCATTCATCAAGCTGAA 63
Qy      21  SerTrpAspAsnValGlyLeuLeuValAluProSerProPronHisThiValAspThrLeu 40
Db      64  TCATGGGATTAATGATGATTTATTAAT--GGTAATGATAAAGTTAAGATATTTACAGATATT 120

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OY	41	PheuhethrhaaspleuthngluuValmetgluValleuGluuylalaasp	60
Db	121	CTGCACAACTCGCTCCGAGGATGTTGTATACCAAGCAATTTGAATTCACAT	180
OY	61	LeuIleuSerYrniSProPciIlePheArProMetlySArGilethrTPraSnthr	80
Db	181	ACCATCTGCTCATCTCATCTATTGTTCAAGAGAAAGCAATTCGTGAAGATGCA	240
OY	81	TrypleSulArGleValIleArGAlaleuGluSnaArGValGlyIleTySerProHis	100
Db	241	TATGCTAGT--ATAATTCGTAACCTTATCCAAATATATATCAATCTTATAGCATTCAC	297
OY	101	ThrlaTyArSpraIaIaIaProGInGlyValaIsnaSnrTPreIuIaIySgIyLeuGlyAla	120
Db	298	ACTAAATCTGTATGTAATTCCTAAAGGATGCAATGTAAGGGATCAATAGTGTTA	357
OY	121	CysThrSerArGrProIleHisProSerLyAlaProAsnTyProThr-----	136
Db	358	GAGAACATATACATGATTAATTAACAATAAGCCATATATATCAAAAGTTCAAACTTTTATA	417
OY	137	-----Glu 137	
Db	418	CCCTAAAAATATATGTAAGATTTCAAGACAGTTTAAACAACTTGGATTAGCTAAAGAA	477
OY	138	GlyAsnHisArGValGluPhe-----AsnValaSnTyThrGln	150
Db	478	GGTAAATTCAGAAATATGTTCTCTTGAAAGTGAAGGCAATTTGGACACATAGT	537
OY	151	AspLeuArSryValMetSerAlaValaIySgIyLeaSpGlyValSerValThrSerPhe	170
Db	538	GATCAAGATCTCTTATATAGGAACTGTAGTATGCAATATGTTGATGAGATATAACTT	597
OY	171	SerAlaArGThrGlyAsnGluGluGlnThrArGleAsnLeuAsnCysThrGlnIySAla	190
Db	598	GAGTTATATGATTAAGAAAGCAATGAA-----TTAGAAATACCTAAACGTCCT	642
OY	191	LeuMetGln-----ValValaSpPheLeuSerArGAsnIySgIn	203
Db	643	ATTTTAAATATATCACCCATACGAAACACACACTTTTGTATTTATTAATTAACAGAAAGAA	702
OY	204	LeuTyGlnIySThrGluIleLeuSerLeuGluIySProLeuLeuLeuHisThrGlyMet	223
Db	703	-----AGGAGTATAGGATTA	717
OY	224	GlyArGleuCysThrLeuAspGluSerValSerLeuAlaThrMetIleArSArgIleIyS	243
Db	718	GGGATTTATGTCACATTAATTAACCAAACTATGACTTATGATGAATTTTGCATATAGCCAAA	777
OY	244	ArgHisLeuIySLeuSerHisIleArGleuAlaLeuGlyValGlyArGThrLeuGluSer	263
Db	778	AAACAGCTCAATATACCGAGCGGTACGAT-----ACAGGTCAACAT--GATAGT	825
OY	264	GlnValIySValAlaIaLeuCysAlaIySerGlySerSerValIleuGlnGlyValGlu	283
Db	826	CCAATTAAGAAAGTAGATCATGAGTGCTCAGGTATA-----GGATTTCAG	873
OY	284	-----AlaAspLeuTyIleuThrGlyGluMetSerHisHisAsp	296
Db	874	TATTAACCTAGCCAACTTGGACGAGATGTTTGTCTACTGGTATATTAACACCATCATAT	933
OY	297	ThrlaAspAlaIaIaSerGInGlyIlaAsnValIleLeuCysGluHisSerAsnThrcIu	316
Db	934	GCTTAAATGCTAAATTCCAAAATGTAAATTTATTAACATCAATCAT--TATATAG	990
OY	317	ArgGlyPheLeuSerAspLeuArGAspMetLeuSerSerHisLeu-----GluAsn	333
Db	991	TATGTTATGAAGAAGGATTAAGAAATATTAAGAAAAAGCTTATTTAAATATGAATAAT	1050
OY	334	LyAlaIeAsnIleIleLeuSerGluThrAspArGAspProLeuGln 346	
Db	1051	CAATTTCCAAATATATGCTTCTGAAATCAACACAGATCCATTTTAAA 1095	

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RESULT 3
US-09-221-017B-610
Sequence 610, Application US/09221017B
Patent No. 6444799
GENERAL INFORMATION:
APPLICANT: Ross, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
NUMBER OF SEQUENCES: 1120
CORRESPONDENCE ADDRESS:
ADDRESSER: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,017B
FILING DATE: 23-DEC-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: P11182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: P11546
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: P29211
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/01023
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAME: Montoy, Gladys H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 27340-20021.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 610:
SEQUENCE CHARACTERISTICS:
LENGTH: 5463 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHEetical: NO
ANTI-SENSE: UNKNOWN
ORIGINAL SOURCE:
ORGANISM: PORPHYROMONAS GINGIVALIS
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1...5463
US-09-221-017B-610

Alignment Scores:
Pred. No.:
Score: 3.05e-20 Length: 5463
Percent Similarity: 253.00 Matches: 94
Best Local Similarity: 43.53% Conservative: 64
Query Match: 25.90% Mismatches: 128
DB: 14.06% Indels: 78
Gaps: 12

US-09-745-506-37 (1-350) x US-09-221-017B-610 (1-5463)

Oy 1 MetAspleuLyalaIeuleuSerLeuAsnAspPheAlaSerLeuSerPheAlaGlu 20
Dh 44 ATGATCATTCAGGATATTTAGAGAGCTATCGAGGCGGTCTGCCAGAGGCTTATCAAGAG 103

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Oy	197	cheuSerAsgAnLysGlnLeuTyrGlnLysThr-----GluLeuSerGln	214
		::: ::: ::: ::: ::: :::	
Db	2503961	GCGATG---CGCGCGCGGACCCCTTACAGAGAGCCGCATTCGACATCTTCGCGCTGT	2503905
Oy	215	LysProLeuLeuLeuHisThrGlyMetCylArgLeuCysThrLeuAspGlnSerValSer	234
		::: ::: ::: ::: ::: :::	
Db	2503904	CCACG---CCGGCGGCGACGCGGTAGCGCGGATTTGGACAGATCGCAAAACCGAACC	2503848
Oy	235	LeuAlaThrMetIleAspArgIleLysArgHisLeuLysLeuSerHisIleArgLeuAla	254
		::: ::: ::: :::	
Db	2503847	CTGGCGACCTTTGTTGCCCGCGCTGTAGAGCCGCGTGGCGCGACT-----GCG	2503800
Oy	255	LeuGlyValGlyArgThrLeuGlnSerGlnValLysVal-----ValAlaLeuCysAla	272
		::: ::: :::	
Db	2503799	ACCGGTGGCGCGCGCGCGGAGATCCGACCTCGTGGTGTGCGGCGTGGCGTGGCGG	2503740
Oy	273	GlySerGlySerSerValLeuGlnGlyValGlnAla-----AspLeuTyrLeuThr	289
		::: ::: ::: :::	
Db	2503739	GCGCGCGGCGCTGTTGGCTTGGCCACCGCTGGCGCGCGCGAGCTGACAGCGTACGTACG	2503680
Oy	290	GlyGluMetSerHisHis-----AspThrLeuAspAlaIleSerGlnGlyIleAsnVal	307
		::: ::: :::	
Db	2503679	GCGCATCTGGCACATCATCCAGCGCAGACAGATTCGCCGAGCTTGGCAA---GTGGCCCTG	2503623
Oy	308	IleLeuCysGlnHisSerAsnThrGluArgGlyPheLeuSerAspLeuAlaGAspMetLeu	327
		::: ::: ::: :::	
Db	2503622	ATCACACGCTCGCGCATTTGGCGAAGCAAAATTCCTCGGTGGCGGCGCGCGCAAGTGTGG	2503563
Oy	328	AspSerHisLeuGlnAsnLysIleAsnIleIleLeuSerGlnThrAspArgAspPro	346
		::: :::	
Db	2503562	CGGTCTCATTTCCGCGCGCTCGCTCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2503506

RESULT 5

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US-08-961-527-33/C
: Sequence 33, Application US/08961527
: Patent No. 6420135
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GENERAL INFORMATION:
: APPLICANT: Charles Kunsch
: TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
: NUMBER OF SEQUENCES: 391
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Human Genome Sciences, Inc.
: STREET: 9410 Key West Avenue
: CITY: Rockville
: STATE: Maryland
: COUNTRY: USA
: ZIP: 20850
:
COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
: COMPUTER: HP Vectra 486/33
: OPERATING SYSTEM: MSDOS version 6.2
: SOFTWARE: ASCII Text
:
CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/961,527
: FILING DATE:
:
CLASSIFICATION: 424
:
PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
:
ATTORNEY/AGENT INFORMATION:
: NAME: Brookes, A. Anders
: REGISTRATION NUMBER: 36,373
: REFERENCE/DOCKET NUMBER: PB340P1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (301) 309-8504
: TELEFAX: (301) 309-8512
:
INFORMATION FOR SEQ ID NO: 33:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 13206 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
:
US-08-961-527-33

```

Alignment Scores:

Presigned Score:	1.91e-13	Length:	13206
Pred. No.:	203.50	Matches:	67
Score:	37.18%	Conservative:	62
Percent Similarity:	19.31%	Mismatches:	121
Best Local Similarity:	11.31%	Indels:	97
Query Match:	4	Gaps:	7
DB:			

US-09-745-506-37 (1-350) x US-08-961-527-33 (1-13206)

[illegible]

```

Db      10793 GATGGGTCTTCGATTGCAGCCAGGTCAC---TATAATCGAAGCATTTTGTAGAAAANA 10737
Qy      323 LeuaIqAspMleUaspsSerHisLseUGluAnslys-----lleasnllleUeu 339
          ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      10736 ATCCGAGCACTTCTTGATGTAATGGAAGAAGATAAAGGGGTGTCTTATGATATCTTGCT 10677
Qy      340 SerGIUthrAsprItraAppro 346
          ||::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      10676 AGTCAGGCATCAACCAATCCT 10656

RESULT 6
US-08-916-421B-1
; Sequence 1, Application US/08916421B
; Patent No. 6503729
GENERAL INFORMATION:
APPLICANT: Built et al.
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanoco
Patent No. 6503729
TITLE OF INVENTION: jannaschl
FILE REFERENCE: PB275
CURRENT APPLICATION NUMBER: US/08/916,421B
CURRENT FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1664976
TYPE: DNA
ORGANISM: Methanococcus jannaschl
FEATURE:
NAME/KEY: misc.feature
LOCATION: (28222)..(28222)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc.feature
LOCATION: (28257)..(28258)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc.feature
LOCATION: (84773)..(84773)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc.feature
LOCATION: (84808)..(84808)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc.feature
LOCATION: (84812)..(84812)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc.feature
LOCATION: (98120)..(98120)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc.feature
LOCATION: (98159)..(98159)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc.feature
LOCATION: (98239)..(98239)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc.feature
LOCATION: (98266)..(98266)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc.feature
LOCATION: (98343)..(98343)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc.feature
LOCATION: (103998)..(103998)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc.feature
LOCATION: (148948)..(148948)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc.feature
LOCATION: (163385)..(163385)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc.feature
LOCATION: (191989)..(191989)
OTHER INFORMATION: n equals a, t, c, or g

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OTHER INFORMATION: n equals a,		t, c, or g
NAME/KEY: misc_feature	LOCATION: (231980) .. (231980)	t, c, or g
OTHER INFORMATION: n equals a,		t, c, or g
NAME/KEY: misc_feature	LOCATION: (234187) .. (234187)	t, c, or g
OTHER INFORMATION: n equals a,		t, c, or g
NAME/KEY: misc_feature	LOCATION: (234220) .. (234220)	t, c, or g
OTHER INFORMATION: n equals a,		t, c, or g
NAME/KEY: misc_feature	LOCATION: (234814) .. (234814)	t, c, or g
OTHER INFORMATION: n equals a,		t, c, or g
NAME/KEY: misc_feature	LOCATION: (309398) .. (309398)	t, c, or g
OTHER INFORMATION: n equals a,		t, c, or g
NAME/KEY: misc_feature	LOCATION: (309418) .. (309418)	t, c, or g
OTHER INFORMATION: n equals a,		t, c, or g
NAME/KEY: misc_feature	LOCATION: (312837) .. (312837)	t, c, or g
OTHER INFORMATION: n equals a,		t, c, or g
NAME/KEY: misc_feature	LOCATION: (312993) .. (312993)	t, c, or g
OTHER INFORMATION: n equals a,		t, c, or g
NAME/KEY: misc_feature	LOCATION: (319226) .. (319226)	t, c, or g
OTHER INFORMATION: n equals a,		t, c, or g
NAME/KEY: misc_feature	LOCATION: (559167) .. (559167)	t, c, or g
OTHER INFORMATION: n equals a,		t, c, or g
NAME/KEY: misc_feature	LOCATION: (559241) .. (559241)	t, c, or g
OTHER INFORMATION: n equals a,		t, c, or g
NAME/KEY: misc_feature	LOCATION: (600992) .. (600992)	t, c, or g
OTHER INFORMATION: n equals a,		t, c, or g
NAME/KEY: misc_feature	LOCATION: (622708) .. (622708)	t, c, or g
OTHER INFORMATION: n equals a,		t, c, or g
NAME/KEY: misc_feature	LOCATION: (657081) .. (657081)	t, c, or g
OTHER INFORMATION: n equals a,		t, c, or g
NAME/KEY: misc_feature	LOCATION: (657203) .. (657203)	t, c, or g
OTHER INFORMATION: n equals a,		t, c, or g
NAME/KEY: misc_feature	LOCATION: (674435) .. (674435)	t, c, or g
OTHER INFORMATION: n equals a,		t, c, or g
NAME/KEY: misc_feature	LOCATION: (682442) .. (682442)	t, c, or g
OTHER INFORMATION: n equals a,		t, c, or g
NAME/KEY: misc_feature	LOCATION: (713652) .. (713652)	t, c, or g
OTHER INFORMATION: n equals a,		t, c, or g
NAME/KEY: misc_feature	LOCATION: (741684) .. (741684)	t, c, or g
OTHER INFORMATION: n equals a,		t, c, or g
NAME/KEY: misc_feature	LOCATION: (779455) .. (779455)	t, c, or g
OTHER INFORMATION: n equals a,		t, c, or g
NAME/KEY: misc_feature	LOCATION: (779676) .. (779676)	t, c, or g
OTHER INFORMATION: n equals a,		t, c, or g
NAME/KEY: misc_feature	LOCATION: (855539) .. (855539)	t, c, or g
OTHER INFORMATION: n equals a,		t, c, or g
NAME/KEY: misc_feature	LOCATION: (871619) .. (871619)	t, c, or g
OTHER INFORMATION: n equals a,		t, c, or g
NAME/KEY: misc_feature		t, c, or g

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LOCATION: (1084830)..(1084830)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1096846)..(1096846)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1119881)..(1119881)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1130881)..(1130881)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1310988)..(1310988)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1313224)..(1313224)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1349473)..(1349473)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1349491)..(1349491)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1470091)..(1470091)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1569020)..(1569020)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1602912)..(1602912)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1603734)..(1603734)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1637998)..(1637998)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc_feature
LOCATION: (1664854)..(1664854)
OTHER INFORMATION: n equals a, t, c, or g
US-08-916-421B-1

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Alignment Scores:
Pred. No.: 2.56e-08 Length: 1664976
Score: 191.00 Matches: 70
Percent Similarity: 38.21% Conservative: 58
Best Local Similarity: 20.90% Mismatches: 111
Query Match: 10.62% Indels: 96
DB: 4 Gaps: 8

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US-09-745-506-37 (1-350) x US-08-916-421B-1 (1-1664976)

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QY 1 MetAspLeuAlaLeuLeuSerSerLeuAsnAspPheAlaSerLeuSerPheAlaGlu 20
DB 614963 ATGAAGAAGCTAAAGAGATTTAAGATTAAAGCTTAAGATTTGCTAAT 615022
QY 21 SerTrpAspAsnValGlyLeuLeuValGluProSerProHisThrValAsnThrLeu 40
DB 615023 GAGGAGATTAACATTTGCTTACAGTTTGACAGACACTTGTGATTAAGATTAAGATTA 615082
QY 41 PheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGlnLysAlaAsp 60
DB 615083 GGTATTTGCTTACAGCTTCAATTAATCAATTAATTAAGATTAAGATTAAGATTA 615142
QY 61 LeuIleLeuSerTyrHisProIlePheArgProMetLysArgIleThrTrpAsnThr 80
DB 615143 TTTTATTTTACCCACCATCTTATTAAGACCCCTATTAAGAAATTTTACGTGAGTTAAT 615202
QY 81 TrpLysGluArgLeuValIleArgAlaLeuGluAsnArgValGlyIleTyrSerProHis 100
DB 615203 TACAAAAAATAAGATTAATTA-----ATGAAATATGACATCATCTCTACTCTGCTCAT 615256

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QY 101 ThrAlaTyrAspAlaIleProGlnGlyValAsnAsnTrpLeuAlaLysGlyLeuGlyAla 120
DB 615257 ACAATTTAGATATATGCAAAAAATGGCTGAATGATGCTTTAGCTGATTAATTAATTA 615316
QY 121 CysThrSerArgProIleHisProSerLysAlaProAsnTyrProThrGluGlnHis 140
DB 615317 GAAATCCAAAGCCCTTA----- 615334
QY 141 ArgValGluPheAsnValAsnTyrThrGlnAspLeuAspLysValMetSerAlaValLys 160
DB 615335 -----TATGATTAATGACCTTGAAGACTT----- 615358
QY 161 GlyIleAspGlyValSerValThrSerPheSerAlaArgThrGlnGlnGluGlnThr 180
DB 615359 -----GCAATTTTAAAGAACTTTTAC----- 615382
QY 181 ArgIleAsnLeuAsnCysThrGlnLysAlaLeuMetGlnValAlaAspPheLeuSerArg 200
DB 615383 -----GAAATTTTGGAGATA 615397
QY 201 AsnLysGlnLeuTyrGlnLysThrGluIleLeuSerLeuGlnLysProLeuLeuHis 220
DB 615398 ACTAAAAAATACATTCACAAAAACCTATTTGTTTAAAGTAA----- 615442
QY 221 ThrGlyMetGlyArgLeuCysThrLeuAspGluSerValSerLeuAlaThrMetIleAsp 240
DB 615443 -----GAGGTACATGACAACTTAAATTTACTGTTTAA----- 615475
QY 241 ArgIleLysArgHisLeuLysLeuSerHisIleArgLeuAlaLeuGlnGlyArgThr 260
DB 615476 -----TCTGTTATATGATTTGCT 615493
QY 261 LeuGluSerGlnValLysValAlaLeuCysAlaGlySerCylSerSerValLeuGln 280
DB 615494 ---CAATCATCCATTAAGATATGCT----- 615517
QY 281 GlyValGluAlaAspLeuTyrLeuThrGlyGluMetSerHisAspThrLeuAspAla 300
DB 615518 ---GAGAAAGCAGATGTCTATCTTCTGGAGATTAAACATCATCTCAAAAAATTTAGCT 615574
QY 301 AlaSerGlnGlyIleAsnValIleLeuCysGlnHisSerAsnThrGluArgIlePheLeu 320
DB 615575 GAGGACCTTGCTTACTGTTGTGTGATGCTACTACTACTCAACTGAAAGTTTGGATTA 615634
QY 321 SerAspLeuArgAspMetLeuAspSerHisLeuGlnLysIle 335
DB 615635 AAGAAATTTAAAGAGTTCTTATCTTCAAAATTTAGATTTAGAAATA 615679

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RESULT 7

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US-09-103-840A-2/c
Sequence 2, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
US-09-103-840A-2

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Oy 142 ValGcluhAasnValaSnYrThrGlnAspLeuAspLysValMetSerAlaValLysGly 161
 Db 408 ----- 408
 Oy 162 IleAspGlyValSerValThrSerPheSerAlaArgThrGlyAsnGlnGlnThrArg 181
 Db 409 -----TCC 411
 Oy 182 IleAsnLeuAsnGlySerThrGlnLysAlaLeuMetGlnValValAspPheLeuSerAlaGAsn 201
 Db 412 ATGCTCTCTCTCGGTTGGCTGGCTGGAGCCAGCATGAGCGCTGCATTCGCTCGGCATGTG 471
 Oy 202 LysGlnLeuValGlyGlnLysThrGlnIleLeuSerLeuGlnLysProLeuLeuLHisThr 221
 Db 472 CGCGATCGCGGTGGGGCGCT-----GAGCGCGCTGCTGTCGATGCC 510
 Oy 222 GlyMetGlyArgLeuGlySerThrLeuAspGlySerValSerLeuAlaThrMetIleAspArg 241
 Db 511 GGT----- 513
 Oy 242 IleValArgHisLeuLysLeuSerHisIleArgLeuAlaLeuGlyValGlyArgThrLeu 261
 Db 513 ----- 513
 Oy 262 GluSerGlnValLysValValAlaLeuCysAlaGlySerGlySerValLeu--Gln 280
 Db 514 ---CAGCCGATCCGGCCGATCGCTGGTGACCGCGCGCCAGGCGCTATATCGACAG 570
 Oy 281 GlyValGluVala-----AspLeuThrLeuThrGlyGluMetSerHisHisAspThrLeu 298
 Db 571 GCGATCGCGCTGGCGCTGCGATGCTTACCTACGACGGAGGTTTCCGAGCAGACCGTGCAC 630
 Oy 299 AspAlaAlaSerGlnGlyIleAsnValIleLeuGlyGlnHisSerAsnThrGluArgGly 318
 Db 631 AGCCGCGGGGAGAGCGCATCAGCTTCATCGCCGCCGACACCATGCCACGAGCGCTAC 690
 Oy 319 PheLeuSerAspLeuArgAspMetLeu 327
 Db 691 GGGGTACAGCGCGTGGCGCACTACTGTG 717
 RESULT 9
 US-09-252-991A-8235/c
 : Sequence 8235, Application US/09252991A
 : Patent No. 6551795
 : GENERAL INFORMATION:
 : APPLICANT: Marc J. Rubenfield et al.
 : TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 : FILE REFERENCE: 107196.136
 : CURRENT APPLICATION NUMBER: US/09/252,991A
 : CURRENT FILING DATE: 1999-02-18
 : PRIOR APPLICATION NUMBER: US 60/074,788
 : PRIOR FILING DATE: 1998-02-18
 : PRIOR APPLICATION NUMBER: US 60/094,190
 : PRIOR FILING DATE: 1998-07-27
 : NUMBER OF SEQ ID NOS: 33142
 : SEQ ID NO 8235
 : LENGTH: 888
 : TYPE: DNA
 : ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-8235

Alignment Scores:

Pred. No.:	0.00241	Length:	888
Score:	106.00	Matches:	63
Percent Similarity:	31.31%	Conservative:	40
Best local Similarity:	19.15%	Mismatches:	124
Query Match:	5.89%	Indels:	102
DB:	4	Gaps:	9

US-09-745-506-37 (1-350) x US-09-252-991A-8235 (1-888)

[illegible]

RESULT 10

US-09-328-352-356
; Sequence 356, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:

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APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: GTC99-03PA
CURRENT FILING DATE: 1999-06-04
CURRENT FILING NUMBER: US/09/328,352
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO: 356
LENGTH: 789
TYPE: DNA
ORGANISM: Acinetobacter baumannii
US-09-328-352-356

Alignment Scores:
Pred. No.: 0.00349 Length: 789
Score: 104.00 Matches: 69
Percent Similarity: 31.22% Conservative: 44
Best Local Similarity: 19.06% Mismatches: 112
Query Match: 5.78% Indels: 137
Gaps: 14

US-09-745-506-37 (1-350) x US-09-328-352-356 (1-789)

QY 6 LeuSerSerLeuAsnAspPheAlaSerPheAlaGluSerTrp---AspAsn 24
DB 10 CTACTCAATTCAGAAATATCATGCAATTTGCAATGATTCAGTGTGCGACCA 69
QY 25 Val-----GlyLeuValGluProSer 32
DB 70 ACCTTAAGCAGCAGATTAAGATTAGCCACCAATGCGCTGCAGAAATTGGAAGTCA 129
QY 33 ProProHisThrValAsnThrLeuPheLeuThrAsnAspLeuThrGluValMetL 52
DB 130 ACT-----GAAGTAAACGATATCTTGTGCAGTACTGCTTGAAGATGCAATTGAT 183
QY 53 GluValLeuGlnLysValAspLeuLeuSerTrpHisProPheArg 71
DB 184 GCACCGATGCTAAGATGATCTCTTACTCGACCCACGCGTATTATTGGAAAGC 243
QY 72 -----PrometLysArgIleThrTrpAsnThrTrpLysGluArgLeuValIleArg 88
DB 244 GAACCGATTCATTAAGTATGATGCGAGTAAACCTATATAA-----AAA 288
QY 89 AlaLeuGluAsnArgValGlyIleYerSerProHisThrAlaIleAlaProGln 108
DB 289 CTATATCAAAATATATCTCATTTAGTCGTTACCATTCGCTTGAATGACATCCGAGT 348
QY 109 ---GlyValAsnAsnTrpLeuAlaLysGlyLeuGlyAlaCysThrSerArgProIle--- 126
DB 349 TTAGCATATATATCCGATATGCGAAGAAACATAAATTACAAATTAGAACCACTTAT 408
QY 127 -----HisProSerLysAlaProAsnTrpProThrGluGlyAsnHisArgVal 142
DB 409 CTAACTGAGAAACATCCCAATTGCT----- 432
QY 143 GluPheAsnValAsnTrpThrGluAspLeuAspLysValMetSerAlaValLysGlyIle 162
DB 433 -----AATATCGGTTATTAGAG----- 450
QY 163 AspGlyValSerValThrSerPheSerAlaArgThrGlyAsnGluGluGlnThrArgIle 182
DB 451 CAAGCGCTTTCTGTAGAGAAATTAAACCAAA----- 483
QY 183 AsnLeuAsnCysThrGlnLysAlaLeuMetGlnValValAspPheLeuSerArgAsnLys 202
DB 484 -----CTACAAAACGGGTTTGATTTT-----AAA 507
QY 203 GlnLeuTrpGlnLysThrGluLeuSerLeuGluLysProLeuLeuHisThrGly 222
DB 508 GTGATCCATTTATACCGCTGAAACAAAGATATTCAAAA----- 546
QY 223 MetGlyArgLeuCysThrLeuAspGluSerValSerLeuAlaThrMetIleAspArgIle 242
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DB 546 ----- 546
QY 243 LysArgHisLeuLysLeuSerHisIleArgLeuAlaLeuGlyValGlyArgThrLeuGlu 262
DB 546 ----- 546
QY 263 SerGlnValLysValAlaAlaLeuCysAlaGlySer-----GlySerSer 277
DB 547 -----GGGGCTTCTGTACAGCGGTCTCAAGATTTTATTTGCTAAAGCT 591
QY 278 ValLeuGlnGlyValGluAlaAspLeuTrpIleThrGluGluMetSerHisAspThr 297
DB 592 GCTTTACAA-----AATGGGATGCTTATATTTACAGCGCAAGTCAAGCAAGCTTT 645
QY 298 LeuAspAlaAlaSerGlnGlyIleAsnValIleLeuCysGlnHisSerAsnThrGluArg 317
DB 646 TATGACGAAAGATTAAGCGTTCAATATTTGCTGCTGTCACACATGCAACCAAGCT 705
QY 318 GlyPheLeuSerAspLeuArgAspMetLeuAspSerHisLeuGluLysIleAsnIle 337
DB 706 TATGGGCTTCAACGTTTACACAAAGCAATTTCAAAACGTTTGCTATTTGAAGTGAATAT 765
QY 337 eile 338
DB 766 TTIG 769

RESULT 11
US-09-146-053-1
Sequence 1, Application US/09146053A
Patent No. 6399349
GENERAL INFORMATION:
APPLICANT: Ryan, James W.
APPLICANT: Sprinkle, Terry Joe Curtis
APPLICANT: Venema, Richard C.
TITLE OF INVENTION: Human AminoPeptidase P Gene
FILE REFERENCE: MCG103
CURRENT APPLICATION NUMBER: US/09/146,053A
EARLIER FILING DATE: 1998-09-02
CURRENT FILING DATE: 1997-09-02
EARLIER APPLICATION NUMBER: 60/057,854
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 3428
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (265)..(2283)
US-09-146-053-1

Alignment Scores:
Pred. No.: 0.1 Length: 3428
Score: 101.00 Matches: 69
Percent Similarity: 35.33% Conservative: 55
Best Local Similarity: 19.66% Mismatches: 123
Query Match: 5.61% Indels: 104
Gaps: 15

US-09-745-506-37 (1-350) x US-09-146-053-1 (1-3428)

QY 20 GluSerTrpAspAsnValGlyLeuLeuValGluProSerProProHisThrValAsnThr 39
DB 734 GACACCTGGAGAGATTAGATCTGCCCTCCAGGCTTAAACAGACAGCTGTGTC- 810
QY 40 LeuPheLeuThrAsnAspLeuThrGluGluValMetGluGluValLeuGlnLysAla 59
DB 811 -----ATCACACCAACATCTGTGACCGGTATGGGA----- 843
QY 60 AspLeuIleLeuSerTrpHisPro-----ProIlePheArgProMetLys 74
DB 844 -----TCAGAGAGCGCCACCGGTTCCAAATCAACCATTTATGCTGACGAG 891
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OY 75 ArgIleThrTrpAsnThrTrpLysGluArgLeuValIleArgAlaLeuGluAsnArgVal 94
Db 892 GCATTACAGAGGAGCACTTGGCAGAGAAAGTA-----TCF 927
OY 95 GlyIleTyrSerProHisThrAlaTyrAspAlaAlaProGlnGlyVal-----110
Db 928 GGGCTCCGAGAGCAGATGCCAGAAAGTCCGAGTCCGCTCTCTGTGTGGCG 987
OY 111 -----AsnAsnTrpLeuAlaLysGlyLeuGlyAlaCysThrSerArgProIleHis 127
Db 988 CTTCGAGAGACGGCTGGCTCTTCAAC-----CTTCA 1020
OY 128 ProSerLysAlaProAsnTyrProThrGlnGluAsnHisArgValGluPheAsnValAsn 147
Db 1021 GCCAGTGCATCCCTCAATAACCC-----TTCTCTATATCC 1056
OY 148 TyrThrGlnAspLeuAspLysValMetSerAlaValLysGlyIleAspGlyValSerVal 167
Db 1057 TACACGCTGCTGCACAC-----TCTTCTATATAGGTTG 1089
OY 168 ThrSerPheSerAlaArgThrGluAsnGlnGluGlnThrArgIleAsnLeuAsnCysThr 187
Db 1090 TTTCGAAACAGAGTGGCTTTAGCTCCGAAACCTTGAGCTATGAACTTCAGTTGCACA 1149
OY 188 GlnLysAlaLeuMetGlnValValAspPhe-----197
Db 1150 GGCCCATGTGTGCAAAATCGAGATTACAGCCAAATTGCTGCACAGCATCCAGGCTAC 1209
OY 198 -----LeuSerArgAsnLysGlnIleTyrGlnLysThrGlu 209
Db 1210 TCATTGGAGATGTGAGATCTGGATTGGACACCATATACCATGTATGCGATGTATGAA 1269
OY 210 IleLeuSerLeuGlnLysProLeuLeuLeuHisThrGlyMetLysArgLysCysThrLeu 229
Db 1270 ATGATACCAAGGAGAAA-----CTCGTG 1293
OY 230 AspGluSerValSerLeuAlaThrMetIleAspArgIleLysArgHis-----245
Db 1294 ACAGAACCTACTGCCAGATGATGACCAAGCAAGCAAGCAAGCAAGCAAGCAAGCC 1353
OY 246 ---LeuLysLeuSerHisIleArgLeuAlaLeuGlyValGlyArg-----ThrLeu 261
Db 1354 CTCCTCAAGGCCCGCCGCGGCGGAGCTGTGCTGATCCGATCTGTGCTGCTG 1413
OY 262 GluSerGlnValLysValAlaAlaLeuCysAlaGlySerGlySerSerValLeuGlnGly 281
Db 1414 GAGAGACGCTGCCAAAGCCACAGATGATGATTTCCGGGCGAAGATCGTGACAAAG 1473
OY 282 ValGluAlaAspLeuTyrLeuThrGlnGluMetSerHisHisAspThrLeuAspAlaAla 301
Db 1474 TTCGAGAGAGAAACAGATTCTCCGAGCCAGT---TTTGAACCATCTCTGCTAGT 1530
OY 302 SerGlnGlyIleAsnValIleLeuCysGlnHisSerAsnThrGlu-----ArgGly 318
Db 1531 ---GGTTTGAATCTGCCCTGGCCCACTACAGCCCGCAAGAGAGTGAAGCCCAAG 1584
OY 319 PheLeuSerAspLeuArgAspMetLeuAspSer 329
Db 1585 CTGTCTCTCAATGAGATGTACTGCTGACTCT 1617

RESULT 12
US-10-002-593-9
; Sequence 9, Application US/10002593
; Patent No. 6586198
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: Brown, Nancy J.
; TITLE OF INVENTION: BIOLOGICAL MARKERS AND DIAGNOSTIC TESTS FOR ANGIOTENSIN CONVERTIN
; TITLE OF INVENTION: INHIBITOR AND VASOPRESSIN INHIBITOR ASSOCIATED ANGIOEDEMA
; FILE REFERENCE: Atty Docket No. 6586198 1242/48/2
; CURRENT APPLICATION NUMBER: US/10/002,593
; PRIOR APPLICATION NUMBER: 60/244,524

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; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 3428
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-002-593-9

Alignment Scores:
Pred. No.: 0.1 Length: 3428
Score: 101.00 Matches: 69
Percent Similarity: 35.33% Conservative: 55
Best Local Similarity: 19.66% Mismatches: 123
Query Match: 5.61% Indels: 104
DB: 4 Gaps: 15

US-09-745-506-37 (1-350) x US-10-002-593-9 (1-3428)
OY 20 GluSerTrpAsnValGlyLeuValGluProSerProHisThrValAsnThr 39
Db 754 GACACCTGGAGAGATATGATCTGGCTCCAAAGCTCTTAACAGACAGCTGTCTCC---810
OY 40 LeuPheLeuThrAsnAspLeuThrGlnGluValMetGlnGluValLeuGlnLysAla 59
Db 811 ---ATCACAAACCAATCTGTGACCTGTGAGGA-----843
OY 60 AspLeuIleLeuSerTyrHisPro-----ProIlePheArgPrometLys 74
Db 844 ---TCAGAGAGCCACCGCTTCCAAATCAACCATTTATATGCCCTGCAGAG 891
OY 75 ArgIleThrTrpAsnThrTrpLysGluArgLeuValIleArgAlaLeuGluAsnArgVal 94
Db 892 GCATTACAGAGGAGCACTTGGCAGAGAAAGTA-----TCF 927
OY 95 GlyIleTyrSerProHisThrAlaTyrAspAlaAlaProGlnGlyVal-----110
Db 928 GGGCTCCGAGAGCAGATGCCAGAAAGTCCGAGTCCGCTCTGTGTGGCG 987
OY 111 -----AsnAsnTrpLeuAlaLysGlyLeuGlyAlaCysThrSerArgProIleHis 127
Db 988 CTTCGAGAGACGGCTGGCTCTTCAAC-----CTTCA 1020
OY 128 ProSerLysAlaProAsnTyrProThrGlnGluAsnHisArgValGluPheAsnValAsn 147
Db 1021 GCCAGTGCATCCCTCAATAACCC-----TTCTCTATATCC 1056
OY 148 TyrThrGlnAspLeuAspLysValMetSerAlaValLysGlyIleAspGlyValSerVal 167
Db 1057 TACACGCTGCTGCACAC-----TCTTCTATATAGGTTG 1089
OY 168 ThrSerPheSerAlaArgThrGluAsnGlnGluGlnThrArgIleAsnLeuAsnCysThr 187
Db 1090 TTTCGAAACAGAGTGGCTTTAGCTCCGAAACCTTGAGCTATGAACTTCAGTTGCACA 1149
OY 188 GlnLysAlaLeuMetGlnValValAspPhe-----197
Db 1150 GGCCCATGTGTGCAAAATCGAGATTACAGCCAAATTGCTGCACAGCATCCAGGCTAC 1209
OY 198 -----LeuSerArgAsnLysGlnIleTyrGlnLysThrGlu 209
Db 1210 TCATTGGAGATGTGAGATCTGGATTGGACACCATATACCATGTATGCGATGTATGAA 1269
OY 210 IleLeuSerLeuGlnLysProLeuLeuLeuHisThrGlyMetLysArgLysCysThrLeu 229
Db 1270 ATGATACCAAGGAGAAA-----CTCGTG 1293
OY 230 AspGluSerValSerLeuAlaThrMetIleAspArgIleLysArgHis-----245
Db 1294 ACAGAACCTACTGCCAGATGATGACCAAGCAAGCAAGCAAGCAAGCAAGCC 1353
OY 246 ---LeuLysLeuSerHisIleArgLeuAlaLeuGlyValGlyArg-----ThrLeu 261
Db 1354 CTCCTCAAGGCCCGCCGCGGCGGAGCTGTGCTGATCCGATCTGTGCTGCTG 1413

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[illegible]

Score:	97.50	Matches:	58
Percent Similarity:	40.64%	Conservative:	444
Best Local Similarity:	23.1%	Mismatches:	83
Query Match:	5.43%	Indels:	67
DB:	4	Gaps:	13

US-09-745-506-37 (1-350) x US-09-252-991A-12362 (1-969)

QY	113	TRPLEuAlaLys61LysuLys1LacysThrSerArgProIleHisProSerLys-----	130
Db	754	TGTTGGGCTTCGGCGTCGACGGCGGTGTCTGGCGAGAGTGTCTGAGAGCCCAACCGGACTG	658
QY	131	-----	AlaProAsn 133
Db	695	GCGGCCCTGCTGGTATCGGCGATCAAGGTCATGCGACGCGCTGCAATGCGAGAGACGT	638
QY	134	TyrProThrGlnGlyAsnHisArgValGluPheAsnValAsnTyrThrGlnAspLeuAsp	153
Db	635	ATTCCCAAGATGGG-----CGGATTTCCCTCGCGGTGGCC-----GGGCGCGAGGTGGAC	585
QY	154	LysValMetSerAlaValLysGlyLeuAspGlyValSerValThrSerPheSerAlaArg	173
Db	584	ATCCGGGTCTCGACCTGCTCCCTCGGCCCAAGGTGAACGGGTGGT-----CTCGGT	534
QY	174	ThrGlyAsnGluGlnGlnThrArgIleAsnLeuAsnGlyThrGlnLysAlaLeuMetGln	193
Db	533	CTGCTCGACACAGAGCGCGGGCGCTGAACCTG-----CA	498
QY	194	ValValAspPheLeuSerArgAsnLysGlnLeuTyrGlnLysThrGluIleLeuSerLeu	213
Db	497	CACCTGGCGATGAGCGACGCGACCGCAAGCTGATGAGACGAACG-----GTG	450
QY	214	GlnLysPro-----LeuLeuLeu-----HisThrGlyMetGlyArgLeuCysThr	228
Db	449	CGCAAGCCCGACGGCATTCCTGCTGTGTACACGGCCCGACCGGCTCGGCGAAGACCAACACC	390
QY	229	Leu-----AspGluSerValSerLeuAlaThrMetIleAsp	240
Db	389	CTTGACGCCAGCTGACACAGCTCAACAGACGGCAGGAAATCTTCACCGTGAAGAT	330
QY	241	ArgIleLysArgHisLeuLysLeuSerHisIleArgLeuAlaLeuGlyValGlyArgThr	260
Db	329	CCGATGGAATACCACTCGTAG-----GGCATCGGCACAGACC	294
QY	261	LeuGluSerGluValLysVal-----ValAlaLeuCysAlaGlySerGlySerValLeu	279
Db	293	-----CAGGTCAACGCCAAGGTGCACATGACCTTCGCCCGCGGCTCGCGGCGCAT	243
QY	280	GlnGlyValGluAlaAspLeuTyrLeuThrGlnGlyMetSerHisAspThrLeuAsp	299
Db	242	CTCCGGCAGAGACCGGACAGCTGGTATGCTGGCGAGATCCCGACCGGAGACCCCGCAG	183
QY	300	AlaAlaSerGln-----GlyIleAsnValIleLeuCysGluHisSerAsnThr	315
Db	182	ATCGCGGTACAGGCTTCGCTGACCGGCAACCTGGTGTCTGACCTGTCAACACCAACAGC	123
QY	316	GluArgGlyPheLeuSerAspLeuArgAspMet	326
Db	122	GCCATCGGTGCATCACCGGCTGTGGACATG	90

RESULT 15
US-09-252-991A-12109
Sequence 12109, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18

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?
? PRIOR APPLICATION NUMBER= US 60/094,190
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? PRIOR FILING DATE= 1998-07-27
?
? NUMBER OF SEQ ID NOS= 33142
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? SEQ ID NO 12109
?
? LENGTH= 1530
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? TYPE= DNA
?
? ORGANISM= Pseudomonas aeruginosa
?
? US-09-253-991A-12109

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Alignment Scores:

Pred. No.:	0.0691	Length:	1530
Score:	97.50	Matches:	58
Percent Similarity:	40.66%	Conservative:	44
Best Local Similarity:	23.11%	Mismatches:	83
Query Match:	5.42%	Indels:	67
DB:	4	Gaps:	13

US-09-745-506-37 (1-350) x US-09-252-991A-12109 (1-1530)

OY	113	TrpLeuAlaLysGlyLeuGlyAlaCysThrSerArgProIleHisProSerLys-----	130
Db	473	TGGTGGCGTTCCGGCGTGCAGCGCGCTGCTGGCGAGGTG-CTGGAGCCCAAGCGCAAGCTG	531
OY	131	-----AlaProAsn	133
Db	532	GCGGCGCTGTGTATGCGCGGATCAATGCGACGCTGGACATGCGCGAGAAGCGT	591
OY	134	TyrProThrGlnGlyAsnHisArgValJalIurPheAsnValAsnTyrThrGlnAspLeuAsp	153
Db	592	ATTTCCCGCCAGATGGG-----CGGATTTTCCCTGGCGGTCGCG- -GGCGCGAGGTGGAC	642
OY	154	LysValIleMetSerAlaValIylsGlyLysArgGlyLysValSerValThrSerPheSerIleArg	173
Db	643	ATCCGCGCTGTGCACCCCTCCCTCGGCCAACGGTGAACGGGTGCTG-----CTGGCT	693
OY	174	ThrGlyAsnGlnGlnGlnThrArgIleAsnLeuAsnCysThrGlnLysAlaLeuMetGln	193
Db	694	CTGCTCGACAGACAGCGCGGCGCGCTGAACCTG-----CA- 729	
OY	194	ValValAspPheLeuSerArgAsnLysGlnLeuTyrGlnLysThrGlnIleLeuSerLeu	213
Db	730	CACTTGGGCAAGACGAGCGCGACCGGACCGCAAGCTGATGGAGCAAGC-----CTG 777	
OY	214	GluLysPro-----LeuLeuLeu-----HisThrGlnMetGlyArgLeuCysThr	228
Db	778	CGCAAGCCGCAAGCGCATCTCTGTGGTCAACCGGCCCCACCGGGTGGGGAAGCAACCAAC	837
OY	229	Leu-----AspGlnSerValSerLeuAlaThrMetLeuAsp	240
Db	838	CTGTAACGGCACCTGCACCAAGCTCAACAGACCGGAGAACATCTCCACGCTCAGAGAT	897
OY	241	ArgIleLysArgHisLeuLysLeuSerHisIleArgLeuAlaLeuGlyValGlyArgThr	260
Db	898	CCGATCGCAATCCACACTGGAG-----GGCATGGCGGCAGAC	933
OY	261	LeuGlnSerGlnValLysVal---ValAlaLeuCysAlaGlySerGlySerSerValLeu	279
Db	934	-----CAGGTTCACGCCAAGGTGCACATGACCTTGGCCCGCGGCGCTGGCGGCGATC	984
OY	280	GlnGlyValGlnAlaAspLeuTyrLeuThrGlnGlnMetSerHisAspThrLeuAsp	299
Db	985	CTCCGGCGACAGCCCGAGACTGTGTATGGTCGCGAGATCCGAGACCGGGAACGCCCGAG	1044
OY	300	AlaAlaSerGln-----GlyIleAsnValIleLeuCysGlnHisSerAsnThr	315
Db	1045	ATTCGCGGTCAGAGCTTGGCTGACCGGACCACTGGGTCCTGGACCTGCACACCAACAGC	1104
OY	316	GlnArgGlyPheLeuSerAspLeuArgAspMet	326
Db	1105	GCCATCTGGTGGATCACCCTGCTGGATGACATGG 1137	

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